



-1-

SEQUENCE LISTING

<110> Umana, Pablo  
Bruenker, Peter  
Ferrara, Claudia  
Suter, Tobias

<120> Fusion Constructs and Use of Same to Produce Antibodies with  
Increased Fc Receptor Binding Affinity and Effector Function

<130> 1975.0180003

<140> US 10/761,435

<141> 2004-01/22

<150> US 60/441,307

<151> 2003-01-22

<150> US 60/491,254

<151> 2003-07-31

<150> US 60/495,142

<151> 2003-08-15

<160> 20

<170> PatentIn version 3.2

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<211> 11

<212> PRT

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<223> c-myc epitope tag

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ttcgg 65

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gtcccc 66

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<210> 10  
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<210> 11  
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<210> 12  
<211> 1715  
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<223> Nucleotide sequence of GnTI-GnTIII

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ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180  
ttgctagctg agaataatga gatcatctca aatattagag actcagtcac caatttgagt 240  
gagtctgtgg aggatggtcc gaaaagttca caaagcaatt tcagccaagg tgctgggtca 300  
ccctgctcc agccactgtc ccctagcaag gccaccgaag aactgcaccg ggtggacttc 360

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aaaccaggta ccaggatgct ggagaaacct tctccagggc ggacagagga gaagaccaag 480
gtggctgagg ggtcctcggg ccgggggtcct gctcggaggc ctatgcggca tgtgttgagt 540
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<210> 13

<211> 571

<212> PRT

<213> Artificial Sequence

<220>

<223> Amino acid sequence of GnTI-GnTIII

<400> 13

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Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp

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Ser	Met	Leu	Gln	Glu	Lys	Ile	Asp	His	Leu	Glu	Arg	Leu	Leu	Ala	Glu
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Asn	Asn	Glu	Ile	Ile	Ser	Asn	Ile	Arg	Asp	Ser	Val	Ile	Asn	Leu	Ser
65					70					75					80
Glu	Ser	Val	Glu	Asp	Gly	Pro	Lys	Ser	Ser	Gln	Ser	Asn	Phe	Ser	Gln
				85					90					95	
Gly	Ala	Gly	Ser	Pro	Leu	Leu	Gln	Pro	Leu	Ser	Pro	Ser	Lys	Ala	Thr
			100					105					110		
Glu	Glu	Leu	His	Arg	Val	Asp	Phe	Val	Leu	Pro	Glu	Asp	Thr	Thr	Glu
		115					120					125			
Tyr	Phe	Val	Arg	Thr	Lys	Ala	Gly	Gly	Val	Cys	Phe	Lys	Pro	Gly	Thr
	130					135					140				
Arg	Met	Leu	Glu	Lys	Pro	Ser	Pro	Gly	Arg	Thr	Glu	Glu	Lys	Thr	Lys
145					150					155					160
Val	Ala	Glu	Gly	Ser	Ser	Val	Arg	Gly	Pro	Ala	Arg	Arg	Pro	Met	Arg
				165					170					175	
His	Val	Leu	Ser	Ala	Arg	Glu	Arg	Leu	Gly	Gly	Arg	Gly	Thr	Arg	Arg
			180					185					190		
Lys	Trp	Val	Glu	Cys	Val	Cys	Leu	Pro	Gly	Trp	His	Gly	Pro	Ser	Cys
		195					200					205			
Gly	Val	Pro	Thr	Val	Val	Gln	Tyr	Ser	Asn	Leu	Pro	Thr	Lys	Glu	Arg
	210					215					220				
Leu	Val	Pro	Arg	Glu	Val	Pro	Arg	Arg	Val	Ile	Asn	Ala	Ile	Asn	Ile
225					230					235					240
Asn	His	Glu	Phe	Asp	Leu	Leu	Asp	Val	Arg	Phe	His	Glu	Leu	Gly	Asp
				245					250					255	
Val	Val	Asp	Ala	Phe	Val	Val	Cys	Glu	Ser	Asn	Phe	Thr	Ala	Tyr	Gly
			260					265					270		

Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly Thr Phe  
275 280 285

Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His Phe Pro  
290 295 300

Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu Arg Thr  
305 310 315 320

Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg Pro Asp  
325 330 335

Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg Asp Gly  
340 345 350

Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe Ala Phe  
355 360 365

His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro Gly Thr  
370 375 380

Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala Val Tyr  
385 390 395 400

Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr Met Pro  
405 410 415

Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val Gln Trp  
420 425 430

Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser Trp Cys  
435 440 445

Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln Asn Gly  
450 455 460

Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu Asn Tyr  
465 470 475 480

Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr Gln Gln  
485 490 495

Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro Lys Tyr  
500 505 510

Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn Pro Tyr  
515 520 525

Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln Gly Ser  
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Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr Glu Gly  
545 550 555 560

Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
565 570

<210> 14  
<211> 1722  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Nucleotide sequence of ManII-GnTIII

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agcgctctcg atggcgaccc cgccagcctc acccggaag tgattcgctt ggcccaagac 180  
gccgaggtgg agctggagcg gcagcgtggg ctgctgcagc agatcgggga tgccctgtcg 240  
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cccgcgcccc tgctccagcc actgtcccct agcaaggcca ccgaagaact gcaccgggtg 360  
gacttcgtgt tgccggagga caccacagag tattttgtgc gcaccaaagc tggcgggtgtg 420  
tgcttcaaac caggtaccag gatgctggag aaaccttctc cagggcggac agaggagaag 480  
accaaggtgg ctgaggggtc ctcggtccgg ggtcctgctc ggaggcctat gcggcatgtg 540  
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tgctgccag gctggcacgg gccagctgc ggggtgccca ctgtggtcca gtattccaac 660  
ctgcccacca aggagcgcct ggtaccagg gaggtgccga ggcgggttat caacgccatc 720  
aacatcaacc atgagttcga cctgctggat gtgcgcttcc atgagctggg cgatgttgtg 780  
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cgtaccttcc tcaccagga tgggtgtctc cgctgcgca acctgcgacc tgatgacgtc 1020  
tttatcatcg acgacgcgga cgagatccct gcgcgtgatg gtgtgctgtt cctcaagctc 1080  
tacgatggct ggacagagcc cttcgccttc catatgcgca agtccctgta tggtttcttt 1140  
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cgccggaacc agggctcaga cggaaggcca tctgctgtca ggggcaagtt ggatacaacg 1680
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<210> 15
<211> 573
<212> PRT
<213> Artificial Sequence

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<220>
<223> Amino acid sequence of ManII-GnTIII fusion
<400> 15

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Met Leu Lys Lys Gln Ser Ala Gly Leu Val Leu Trp Gly Ala Ile Leu
1           5           10           15

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```

Phe Val Ala Trp Asn Ala Leu Leu Leu Phe Phe Trp Thr Arg Pro
20           25           30

```

```

Ala Pro Gly Arg Pro Pro Ser Val Ser Ala Leu Asp Gly Asp Pro Ala
35           40           45

```

```

Ser Leu Thr Arg Glu Val Ile Arg Leu Ala Gln Asp Ala Glu Val Glu
50           55           60

```

```

Leu Glu Arg Gln Arg Gly Leu Leu Gln Gln Ile Gly Asp Ala Leu Ser
65           70           75           80

```

```

Ser Gln Arg Gly Arg Val Pro Thr Ala Ala Pro Pro Ala Gln Pro Arg
85           90           95

```

```

Val Pro Val Thr Pro Ala Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys
100          105          110

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```

Ala Thr Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr
115          120          125

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Thr Glu Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro

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Met	Arg	His	Val	Leu	Ser	Ala	Arg	Glu	Arg	Leu	Gly	Gly	Arg	Gly	Thr
			180					185					190		
Arg	Arg	Lys	Trp	Val	Glu	Cys	Val	Cys	Leu	Pro	Gly	Trp	His	Gly	Pro
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Ser	Cys	Gly	Val	Pro	Thr	Val	Val	Gln	Tyr	Ser	Asn	Leu	Pro	Thr	Lys
	210					215					220				
Glu	Arg	Leu	Val	Pro	Arg	Glu	Val	Pro	Arg	Arg	Val	Ile	Asn	Ala	Ile
225					230					235					240
Asn	Ile	Asn	His	Glu	Phe	Asp	Leu	Leu	Asp	Val	Arg	Phe	His	Glu	Leu
				245					250					255	
Gly	Asp	Val	Val	Asp	Ala	Phe	Val	Val	Cys	Glu	Ser	Asn	Phe	Thr	Ala
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Tyr	Gly	Glu	Pro	Arg	Pro	Leu	Lys	Phe	Arg	Glu	Met	Leu	Thr	Asn	Gly
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Thr	Phe	Glu	Tyr	Ile	Arg	His	Lys	Val	Leu	Tyr	Val	Phe	Leu	Asp	His
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Arg	Thr	Phe	Leu	Thr	Gln	Asp	Gly	Val	Ser	Arg	Leu	Arg	Asn	Leu	Arg
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Pro	Asp	Asp	Val	Phe	Ile	Ile	Asp	Asp	Ala	Asp	Glu	Ile	Pro	Ala	Arg
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Asp	Gly	Val	Leu	Phe	Leu	Lys	Leu	Tyr	Asp	Gly	Trp	Thr	Glu	Pro	Phe
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Ala	Phe	His	Met	Arg	Lys	Ser	Leu	Tyr	Gly	Phe	Phe	Trp	Lys	Gln	Pro
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385 390 395 400

Val Tyr Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr  
405 410 415

Met Pro Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val  
420 425 430

Gln Trp Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser  
435 440 445

Trp Cys Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln  
450 455 460

Asn Gly Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu  
465 470 475 480

Asn Tyr Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr  
485 490 495

Gln Gln Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro  
500 505 510

Lys Tyr Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn  
515 520 525

Pro Tyr Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln  
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Gly Ser Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr  
545 550 555 560

Glu Gly Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu  
565 570

<210> 16  
<211> 398  
<212> PRT  
<213> Unknown

<220>  
<223> GalT amino acid sequence from pBlueGalT

<400> 16

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His	Leu	Gly	Val	Thr	Leu	Val	Tyr	Tyr	Leu	Ala	Gly	Arg	Asp	Leu	Ser	35	40	45	
Arg	Leu	Pro	Gln	Leu	Val	Gly	Val	Ser	Thr	Pro	Leu	Gln	Gly	Gly	Ser	50	55	60	
Asn	Ser	Ala	Ala	Ala	Ile	Gly	Gln	Ser	Ser	Gly	Glu	Leu	Arg	Thr	Gly	65	70	75	80
Gly	Ala	Arg	Pro	Pro	Pro	Pro	Leu	Gly	Ala	Ser	Ser	Gln	Pro	Arg	Pro	85	90	95	
Gly	Gly	Asp	Ser	Ser	Pro	Val	Val	Asp	Ser	Gly	Pro	Gly	Pro	Ala	Ser	100	105	110	
Asn	Leu	Thr	Ser	Val	Pro	Val	Pro	His	Thr	Thr	Ala	Leu	Ser	Leu	Pro	115	120	125	
Ala	Cys	Pro	Glu	Glu	Ser	Pro	Leu	Leu	Val	Gly	Pro	Met	Leu	Ile	Glu	130	135	140	
Phe	Asn	Met	Pro	Val	Asp	Leu	Glu	Leu	Val	Ala	Lys	Gln	Asn	Pro	Asn	145	150	155	160
Val	Lys	Met	Gly	Gly	Arg	Tyr	Ala	Pro	Arg	Asp	Cys	Val	Ser	Pro	His	165	170	175	
Lys	Val	Ala	Ile	Ile	Ile	Pro	Phe	Arg	Asn	Arg	Gln	Glu	His	Leu	Lys	180	185	190	
Tyr	Trp	Leu	Tyr	Tyr	Leu	His	Pro	Val	Leu	Gln	Arg	Gln	Gln	Leu	Asp	195	200	205	
Tyr	Gly	Ile	Tyr	Val	Ile	Asn	Gln	Ala	Gly	Asp	Thr	Ile	Phe	Asn	Arg	210	215	220	
Ala	Lys	Leu	Leu	Asn	Val	Gly	Phe	Gln	Glu	Ala	Leu	Lys	Asp	Tyr	Asp	225	230	235	240
Tyr	Thr	Cys	Phe	Val	Phe	Ser	Asp	Val	Asp	Leu	Ile	Pro	Met	Asn	Asp	245	250	255	
His	Asn	Ala	Tyr	Arg	Cys	Phe	Ser	Gln	Pro	Arg	His	Ile	Ser	Val	Ala	260	265	270	

Met Asp Lys Phe Gly Phe Ser Leu Pro Tyr Val Gln Tyr Phe Gly Gly  
275 285

Val Ser Ala Leu Ser Lys Gln Gln Phe Leu Thr Ile Asn Gly Phe Pro  
290 295 300

Asn Asn Tyr Trp Gly Trp Gly Gly Glu Asp Asp Asp Ile Phe Asn Arg  
305 310 315 320

Leu Val Phe Arg Gly Met Ser Ile Ser Arg Pro Asn Ala Val Val Gly  
325 330 335

Arg Cys Arg Met Ile Arg His Ser Arg Asp Lys Lys Asn Glu Pro Asn  
340 345 350

Pro Gln Arg Phe Asp Arg Ile Ala His Thr Lys Glu Thr Met Leu Ser  
355 360 365

Asp Gly Leu Asn Ser Leu Thr Tyr Gln Val Leu Asp Val Gln Arg Tyr  
370 375 380

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<211> 3435  
<212> DNA  
<213> Homo sapiens

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aagtgggtggg atattataga tattcagaag aaggatgctg ttaaaagtgtt aatagaaaat 720

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Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp  
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Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu  
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu  
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser  
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln  
85 90 95

Gly Ala Gly Ser His Leu Leu Pro Ser Gln Leu Ser Leu Ser Val Asp  
100 105 110

Thr Ala Asp Cys Leu Phe Ala Ser Gln Ser Gly Ser His Asn Ser Asp  
115 120 125

Val Gln Met Leu Asp Val Tyr Ser Leu Ile Ser Phe Asp Asn Pro Asp  
130 135 140

Gly Gly Val Trp Lys Gln Gly Phe Asp Ile Thr Tyr Glu Ser Asn Glu  
145 150 155 160

Trp Asp Thr Glu Pro Leu Gln Val Phe Val Val Pro His Ser His Asn  
165 170 175

Asp Pro Gly Trp Leu Lys Thr Phe Asn Asp Tyr Phe Arg Asp Lys Thr  
180 185 190

Gln Tyr Ile Phe Asn Asn Met Val Leu Lys Leu Lys Glu Asp Ser Arg  
195 200 205

Arg Lys Phe Ile Trp Ser Glu Ile Ser Tyr Leu Ser Lys Trp Trp Asp  
210 215 220

Ile Ile Asp Ile Gln Lys Lys Asp Ala Val Lys Ser Leu Ile Glu Asn  
225 230 235 240

Gly Gln Leu Glu Ile Val Thr Gly Gly Trp Val Met Pro Asp Glu Ala  
245 250 255

Thr Pro His Tyr Phe Ala Leu Ile Asp Gln Leu Ile Glu Gly His Gln  
260 265 270

Trp Leu Glu Asn Asn Ile Gly Val Lys Pro Arg Ser Gly Trp Ala Ile  
275 280 285

Asp Pro Phe Gly His Ser Pro Thr Met Ala Tyr Leu Leu Asn Arg Ala  
290 295 300

Gly Leu Ser His Met Leu Ile Gln Arg Val His Tyr Ala Val Lys Lys  
305 310 315 320

His Phe Ala Leu His Lys Thr Leu Glu Phe Phe Trp Arg Gln Asn Trp  
325 330 335

Asp	Leu	Gly	Ser	Val	Thr	Asp	Ile	Leu	Cys	His	Met	Met	Pro	Phe	Tyr	340	345	350	
Ser	Tyr	Asp	Ile	Pro	His	Thr	Cys	Gly	Pro	Asp	Pro	Lys	Ile	Cys	Cys	355	360	365	
Gln	Phe	Asp	Phe	Lys	Arg	Leu	Pro	Gly	Gly	Arg	Phe	Gly	Cys	Pro	Trp	370	375	380	
Gly	Val	Pro	Pro	Glu	Thr	Ile	His	Pro	Gly	Asn	Val	Gln	Ser	Arg	Ala	385	390	395	400
Arg	Met	Leu	Leu	Asp	Gln	Tyr	Arg	Lys	Lys	Ser	Lys	Leu	Phe	Arg	Thr	405	410	415	
Lys	Val	Leu	Leu	Ala	Pro	Leu	Gly	Asp	Asp	Phe	Arg	Tyr	Cys	Glu	Tyr	420	425	430	
Thr	Glu	Trp	Asp	Leu	Gln	Phe	Lys	Asn	Tyr	Gln	Gln	Leu	Phe	Asp	Tyr	435	440	445	
Met	Asn	Ser	Gln	Ser	Lys	Phe	Lys	Val	Lys	Ile	Gln	Phe	Gly	Thr	Leu	450	455	460	
Ser	Asp	Phe	Phe	Asp	Ala	Leu	Asp	Lys	Ala	Asp	Glu	Thr	Gln	Arg	Asp	465	470	475	480
Lys	Gly	Gln	Ser	Met	Phe	Pro	Val	Leu	Ser	Gly	Asp	Phe	Phe	Thr	Tyr	485	490	495	
Ala	Asp	Arg	Asp	Asp	His	Tyr	Trp	Ser	Gly	Tyr	Phe	Thr	Ser	Arg	Pro	500	505	510	
Phe	Tyr	Lys	Arg	Met	Asp	Arg	Ile	Met	Glu	Ser	His	Leu	Arg	Ala	Ala	515	520	525	
Glu	Ile	Leu	Tyr	Tyr	Phe	Ala	Leu	Arg	Gln	Ala	His	Lys	Tyr	Lys	Ile	530	535	540	
Asn	Lys	Phe	Leu	Ser	Ser	Ser	Leu	Tyr	Thr	Ala	Leu	Thr	Glu	Ala	Arg	545	550	555	560
Arg	Asn	Leu	Gly	Leu	Phe	Gln	His	His	Asp	Ala	Ile	Thr	Gly	Thr	Ala	565	570	575	
Lys	Asp	Trp	Val	Val	Val	Asp	Tyr	Gly	Thr	Arg	Leu	Phe	His	Ser	Leu	580	585	590	



Met Val Leu Glu Lys Ile Ile Gly Asn Ser Ala Phe Leu Leu Ile Leu  
595 600 605

Lys Asp Lys Leu Thr Tyr Asp Ser Tyr Ser Pro Asp Thr Phe Leu Glu  
610 615 620

Met Asp Leu Lys Gln Lys Ser Gln Asp Ser Leu Pro Gln Lys Asn Ile  
625 630 635 640

Ile Arg Leu Ser Ala Glu Pro Arg Tyr Leu Val Val Tyr Asn Pro Leu  
645 650 655

Glu Gln Asp Arg Ile Ser Leu Val Ser Val Tyr Val Ser Ser Pro Thr  
660 665 670

Val Gln Val Phe Ser Ala Ser Gly Lys Pro Val Glu Val Gln Val Ser  
675 680 685

Ala Val Trp Asp Thr Ala Asn Thr Ile Ser Glu Thr Ala Tyr Glu Ile  
690 695 700

Ser Phe Arg Ala His Ile Pro Pro Leu Gly Leu Lys Val Tyr Lys Ile  
705 710 715 720

Leu Glu Ser Ala Ser Ser Asn Ser His Leu Ala Asp Tyr Val Leu Tyr  
725 730 735

Lys Asn Lys Val Glu Asp Ser Gly Ile Phe Thr Ile Lys Asn Met Ile  
740 745 750

Asn Thr Glu Glu Gly Ile Thr Leu Glu Asn Ser Phe Val Leu Leu Arg  
755 760 765

Phe Asp Gln Thr Gly Leu Met Lys Gln Met Met Thr Lys Glu Asp Gly  
770 775 780

Lys His His Glu Val Asn Val Gln Phe Ser Trp Tyr Gly Thr Thr Ile  
785 790 795 800

Lys Arg Asp Lys Ser Gly Ala Tyr Leu Phe Leu Pro Asp Gly Asn Ala  
805 810 815

Lys Pro Tyr Val Tyr Thr Thr Pro Pro Phe Val Arg Val Thr His Gly  
820 825 830

Arg Ile Tyr Ser Glu Val Thr Cys Phe Phe Asp His Val Thr His Arg  
835 840 845

Val Arg Leu Tyr His Ile Gln Gly Ile Glu Gly Gln Ser Val Glu Val  
850 855 860

Ser Asn Ile Val Asp Ile Arg Lys Val Tyr Asn Arg Glu Ile Ala Met  
865 870 875 880

Lys Ile Ser Ser Asp Ile Lys Ser Gln Asn Arg Phe Tyr Thr Asp Leu  
885 890 895

Asn Gly Tyr Gln Ile Gln Pro Arg Met Thr Leu Ser Lys Leu Pro Leu  
900 905 910

Gln Ala Asn Val Tyr Pro Met Thr Thr Met Ala Tyr Ile Gln Asp Ala  
915 920 925

Lys His Arg Leu Thr Leu Leu Ser Ala Gln Ser Leu Gly Val Ser Ser  
930 935 940

Leu Asn Ser Gly Gln Ile Glu Val Ile Met Asp Arg Arg Leu Met Gln  
945 950 955 960

Asp Asp Asn Arg Gly Leu Glu Gln Gly Ile Gln Asp Asn Lys Ile Thr  
965 970 975

Ala Asn Leu Phe Arg Ile Leu Leu Glu Lys Arg Ser Ala Val Asn Thr  
980 985 990

Glu Glu Glu Lys Lys Ser Val Ser Tyr Pro Ser Leu Leu Ser His Ile  
995 1000 1005

Thr Ser Ser Leu Met Asn His Pro Val Ile Pro Met Ala Asn Lys  
1010 1015 1020

Phe Phe Ser Pro Thr Leu Glu Leu Gln Gly Glu Phe Ser Pro Leu  
1025 1030 1035

Gln Ser Ser Leu Pro Cys Asp Ile His Leu Val Asn Leu Arg Thr  
1040 1045 1050

Ile Gln Ser Lys Val Gly Asn Gly His Ser Asn Glu Ala Ala Leu  
1055 1060 1065

Ile Leu His Arg Lys Gly Phe Asp Cys Arg Phe Ser Ser Lys Gly  
1070 1075 1080

Thr Gly Leu Phe Cys Ser Thr Thr Gln Gly Lys Ile Leu Val Gln  
1085 1090 1095

Lys Leu Leu Asn Lys Phe Ile Val Glu Ser Leu Thr Pro Ser Ser  
1100 1105 1110

Leu Ser Leu Met His Ser Pro Pro Gly Thr Gln Asn Ile Ser Glu  
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Ile Asn Leu Ser Pro Met Glu Ile Ser Thr Phe Arg Ile Gln Leu  
1130 1135 1140

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Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp  
20 25 30

Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu  
35 40 45

Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu  
50 55 60

Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser  
65 70 75 80

Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln  
85 90 95

Gly Ala Gly Ser Pro Ala Cys Pro Glu Glu Ser Pro Leu Leu Val Gly  
100 105 110

Pro Met Leu Ile Glu Phe Asn Met Pro Val Asp Leu Glu Leu Val Ala  
115 120 125

Lys Gln Asn Pro Asn Val Lys Met Gly Gly Arg Tyr Ala Pro Arg Asp  
130 135 140

Cys Val Ser Pro His Lys Val Ala Ile Ile Ile Pro Phe Arg Asn Arg  
145 150 155 160

Gln Glu His Leu Lys Tyr Trp Leu Tyr Tyr Leu His Pro Val Leu Gln  
165 170 175

Arg Gln Gln Leu Asp Tyr Gly Ile Tyr Val Ile Asn Gln Ala Gly Asp

[illegible]